



SEQUENCE LISTING

<110> Dale Umetsu
Rosemarie DeKruyff
Jennifer McIntire
Gordon Freeman

<120> T CELL REGULATORY GENES ASSOCIATED WITH
IMMUNE DISEASE

<130> STAN-235CIP

<150> 60/302,344

<151> 2001-06-29

<150> 10/188,012

<151> 2002-07-01

<160> 53

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 305

<212> PRT

<213> M. musculus

<220>

<221> VARIANT

<222> (1)...(305)

<223> TIM-1 BALB/c allele

<400> 1

Met	Asn	Gln	Ile	Gln	Val	Phe	Ile	Ser	Gly	Leu	Ile	Leu	Leu	Leu	Pro
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			20					25					30		
Val	Thr	Leu	Pro	Cys	Thr	Tyr	Ser	Thr	Tyr	Arg	Gly	Ile	Thr	Thr	Thr
		35					40					45			
Cys	Trp	Gly	Arg	Gly	Gln	Cys	Pro	Ser	Ser	Ala	Cys	Gln	Asn	Thr	Leu
	50					55					60				
Ile	Trp	Thr	Asn	Gly	His	Arg	Val	Thr	Tyr	Gln	Lys	Ser	Ser	Arg	Tyr
65					70					75				80	
Asn	Leu	Lys	Gly	His	Ile	Ser	Glu	Gly	Asp	Val	Ser	Leu	Thr	Ile	Glu
				85					90					95	
Asn	Ser	Val	Glu	Ser	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Arg	Val	Glu	Ile
			100					105					110		
Pro	Gly	Trp	Phe	Asn	Asp	Gln	Lys	Val	Thr	Phe	Ser	Leu	Gln	Val	Lys
	115						120					125			
Pro	Glu	Ile	Pro	Thr	Arg	Pro	Pro	Thr	Arg	Pro	Thr	Thr	Thr	Arg	Pro
	130					135					140				
Thr	Ala	Thr	Gly	Arg	Pro	Thr	Thr	Ile	Ser	Thr	Arg	Ser	Thr	His	Val
145					150					155				160	
Pro	Thr	Ser	Ile	Arg	Val	Ser	Thr	Ser	Thr	Pro	Pro	Thr	Ser	Thr	His
				165					170					175	
Thr	Trp	Thr	His	Lys	Pro	Glu	Pro	Thr	Thr	Phe	Cys	Pro	His	Glu	Thr
			180					185					190		
Thr	Ala	Glu	Val	Thr	Gly	Ile	Pro	Ser	His	Thr	Pro	Thr	Asp	Trp	Asn
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Gly	Thr	Val	Thr	Ser	Ser	Gly	Asp	Thr	Trp	Ser	Asn	His	Thr	Glu	Ala

210		215		220
Ile Pro Pro Gly Lys	Pro Gln Lys Asn Pro Thr	Lys Gly Phe Tyr Val		
225	230	235	240	
Gly Ile Cys Ile Ala	Ala Leu Leu Leu Leu	Leu Val Ser Thr Val		
	245	250	255	
Ala Ile Thr Arg Tyr	Ile Leu Met Lys Arg Lys	Ser Ala Ser Leu Ser		
	260	265	270	
Val Val Ala Phe Arg	Val Ser Lys Ile Glu Ala	Leu Gln Asn Ala Ala		
	275	280	285	
Val Val His Ser Arg	Ala Glu Asp Asn Ile Tyr	Ile Val Glu Asp Arg		
	290	295	300	
Pro				
305				

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 <211> 918
 <212> DNA
 <213> Mus musculus

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 acatatcgtg gaatcacaaac gacatgttgg ggccgagggc aatgcccatc ttctgcttgt 180
 caaaatacac ttatttggac caatggacat cgtgtcacct atcagaagag cagtcggtac 240
 aacttaaagg ggcataatttc agaaggagat gtgtccttga cgatagagaa ctctgttgag 300
 agtgacagtg gtctgtattg ttgtcgagtg gagattcctg gatggtttaa tgatcagaaa 360
 gtgacctttt cattgcaagt taaaccagag attcccacac gtctccaac aagaccaca 420
 actacaaggc ccacagctac aggaagaccc acgactatct caacaagatc cacacatgta 480
 ccaacatcaa tcagagtctc tacctccact cctccaacat ctacacacac atggactcac 540
 aaaccagaac ccactacatt ttgtcccat gagacaacag ctgaggtgac aggaatccca 600
 tcccatactc ctacagactg gaatggcact gtgacatcct caggagatac ctggagtaat 660
 cacactgaag caatccctcc aggggaagccg cagaaaaacc ctactaaggg cttctatgtt 720
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 tacatactta tgaaggaa gtcagcatct ctaagcgtgg ttgccttcg tgtctctaag 840
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<210> 3
 <211> 282
 <212> PRT
 <213> Mus musculus

<220>
 <221> VARIANT
 <222> (1)...(282)
 <223> TIM-1, C.D2 ES-HBA and DBA/2J allele

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 20 25 30
 Val Thr Leu Pro Cys Thr Tyr Ser Thr Tyr Arg Gly Ile Thr Thr Thr
 35 40 45
 Cys Trp Gly Arg Gly Gln Cys Pro Ser Ser Ala Cys Gln Asn Thr Leu
 50 55 60
 Ile Trp Thr Asn Gly His Arg Val Thr Tyr Gln Lys Ser Ser Arg Tyr
 65 70 75 80
 Asn Leu Lys Gly His Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu
 85 90 95

Asn	Ser	Val	Glu	Ser	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Arg	Val	Glu	Ile
		100						105					110		
Pro	Gly	Trp	Phe	Asn	Asp	Gln	Lys	Val	Thr	Phe	Ser	Leu	Gln	Val	Lys
		115					120					125			
Pro	Glu	Ile	Pro	Thr	Arg	Pro	Pro	Arg	Arg	Pro	Thr	Thr	Thr	Arg	Pro
		130				135					140				
Thr	Ala	Thr	Gly	Arg	Pro	Thr	Thr	Ile	Ser	Thr	Arg	Ser	Thr	His	Val
145					150					155				160	
Pro	Thr	Ser	Thr	Arg	Val	Ser	Thr	Ser	Thr	Pro	Pro	Thr	Ser	Thr	His
				165				170					175		
Thr	Trp	Thr	His	Lys	Pro	Asp	Trp	Asn	Gly	Thr	Val	Thr	Ser	Ser	Gly
			180					185				190			
Asp	Thr	Trp	Ser	Asn	His	Thr	Glu	Ala	Ile	Pro	Pro	Gly	Lys	Pro	Gln
		195					200					205			
Lys	Asn	Pro	Thr	Lys	Gly	Phe	Tyr	Val	Gly	Ile	Cys	Ile	Ala	Ala	Leu
	210					215					220				
Leu	Leu	Leu	Leu	Leu	Val	Ser	Thr	Val	Ala	Ile	Thr	Arg	Tyr	Ile	Leu
225					230					235				240	
Met	Lys	Arg	Lys	Ser	Ala	Ser	Leu	Ser	Val	Val	Ala	Phe	Arg	Val	Ser
				245				250						255	
Lys	Ile	Glu	Ala	Leu	Gln	Asn	Ala	Ala	Val	Val	His	Ser	Arg	Ala	Glu
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Asp	Asn	Ile	Tyr	Ile	Val	Glu	Asp	Arg	Pro						
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<210> 4
 <211> 849
 <212> DNA
 <213> Mus musculus

<400> 4
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 acatatcgtg gaatcacaac gacatgttgg ggccgagggc aatgcccatc ttctgcttgg 180
 caaaatacac ttatttggac caatggacat cgtgtcacct atcagaagag cagtcggtac 240
 aacttaaagg ggcataatttc agaaggagat gtgtccttga cgatagagaa ctctgtttgag 300
 agtgacagtg gtctgtattg ttgtcgagtg gagattcctg gatggtttaa tgatcagaaa 360
 gtgacctttt cattgcaagt taaaccagag attcccacac gtccctccaag aagaccacac 420
 actacaaggc ccacagctac aggaagaccc acgactattt caacaagatc cacacatgta 480
 ccaacatcaa ccagagtctc tacctccact cctccaacat ctacacacac atggactcac 540
 aaaccagact ggaatggcac tgtgacatcc tcaggagata cctggagtaa tcacactgaa 600
 gcaatccctc caggggaagg gcagaaaaaac cctactaagg gcttctatgt tggcatctgc 660
 atcgcagccc tgctgtact gctccttgtg agcacggtgg ctatcaccag gtacatactt 720
 atgaaaagga agtcagcatc tctaagcgtg gttgccttcc gtgtctctaa gattgaagct 780
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 agaccttga 849

<210> 5
 <211> 305
 <212> PRT
 <213> Mus musculus

<220>
 <221> VARIANT
 <222> (1)...(305)
 <223> TIM-2 BALB/c allele

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 Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
 35 40 45
 Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
 50 55 60
 Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg
 65 70 75 80
 Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile
 85 90 95
 Glu Asn Thr Val Val Gly Asp Gly Gly Pro Tyr Cys Cys Val Val Glu
 100 105 110
 Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro
 115 120 125
 Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro
 130 135 140
 Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val
 145 150 155 160
 Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro
 165 170 175
 Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu
 180 185 190
 Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser
 195 200 205
 Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro
 210 215 220
 Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala
 225 230 235 240
 Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val
 245 250 255
 Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile
 260 265 270
 Ser Lys Ile Gly Ala Ser Pro Lys Lys Val Val Glu Arg Thr Arg Cys
 275 280 285
 Glu Asp Gln Val Tyr Ile Ile Glu Asp Thr Pro Tyr Pro Glu Glu Glu
 290 295 300
 Ser
 305

<210> 6
 <211> 958
 <212> DNA
 <213> Mus musculus

<400> 6
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 tcaccctgtc acacttccat gtatttattc gacacacctt ggtggaatcg ttcctatgtg 180
 ttggggccta ggggaatgcc gccattctta ttgtatacgg tcacttatct ggaccaatgg 240
 atatacggtc acacatcaga ggaacagtcg ataccagcta aaggggaata tttcagaagg 300
 aaatgtgtcc ttgaccatag agaacactgt tgtgggtgat ggtgggtccct attgctgtgt 360
 agtggagata cctggagcgt tccattttgt ggactatatg ttggaagtta aaccagaaat 420
 ttccacgagt ccaccaacaa ggcccacagc tacaggaaga cccacaacta tttcaacaag 480
 atccacacat gtaccaacat caaccagagt ctctacctct acttctccaa caccagcaca 540
 cacagagacc tacaacaccag aggccactac attttatcca gatcagacta cagctgaggt 600
 gacagaaacc ttaccctcta ctctgcaga ctggcataac actgtgacat cctcagatga 660
 cccttgggat gataacactg aagtaatccc tccacagaag ccacagaaaa acctgaataa 720
 gggcttctat gttggcatct ccattgcagc cctgctgata ttgatgcttc tgagcaccat 780
 ggttatcacc aggtacgtgg ttatgaaaag gaagtcagaa tctctgagct ttgttgctt 840
 ccctatctct aagattggag cttcccccaa aaaagtggtc gaacggacca gatgtgaaga 900

ccaggtctac attattgaag acactcctta ccctgaagaa gagtcctagt gcctctac 958

<210> 7

<211> 305

<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> (1)...(305)

<223> TIM-2, C.D2 ES-HBA and DBA/2J allele

<400> 7

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Met Asn Gln Ile Gln Val Phe Ile Ser Gly Leu Ile Leu Leu Leu Pro
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Gly Ala Val Glu Ser His Thr Ala Val Gln Gly Leu Ala Gly His Pro
 20          25          30
Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
 35          40          45
Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
 50          55          60
Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg
 65          70          75          80
Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile
 85          90          95
Glu Asn Thr Val Val Gly Asp Gly Gly Pro Tyr Cys Cys Val Val Glu
100          105          110
Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro
115          120          125
Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro
130          135          140
Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val
145          150          155          160
Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro
165          170          175
Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu
180          185          190
Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser
195          200          205
Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro
210          215          220
Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala
225          230          235          240
Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val
245          250          255
Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile
260          265          270
Ser Lys Ile Gly Ala Ser Pro Lys Lys Val Val Glu Arg Thr Arg Cys
275          280          285
Glu Asp Gln Val Tyr Ile Ile Glu Asp Thr Pro Tyr Pro Glu Glu Glu
290          295          300
Ser
305

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<210> 8

<211> 958

<212> DNA

<213> Mus musculus

<400> 8

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tcaccctgtc acacttccat gtattttattc gacacacctt ggtggaatcg ttcctatgtg 180
ttggggccta ggggaatgcc gccattctta ttgtatacgg tcacttatct ggaccaatgg 240
atatacggtc acacatcaga ggaacagtcg ataccagcta aaggggaata tttcagaagg 300
aaatgtgtcc ttgaccatag agaacactgt tgtgggtgat ggtggtcctt attgctgtgt 360
agtggagata cctggagcgt tccattttgt ggactatatg ttggaagtta aaccagaaat 420
ttccacgagt ccaccaacaa ggcccacagc tacaggaaga cccacaacta tttcaacaag 480
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ccctatctct aagattggag cttcccccaa aaaagtggtc gaacggacca gatgtgaaga 900
ccaggtctac attattgaag acactcctta ccccgaagaa gagtcttagt gcctctac 958

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<210> 9

<211> 281

<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> (1)...(281)

<223> TIM-3 BALB/c allele

<400> 9

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          20           25           30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Pro Thr Ser Gly Thr Leu
      35           40           45
Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
      50           55           60
Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
65           70           75           80
Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
          85           90           95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
          100          105          110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
          115          120          125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
      130          135          140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
145          150          155          160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
          165          170          175
Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
          180          185          190
Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu
      195          200          205
Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys Lys
      210          215          220
Leu Ser Ser Leu Ser Leu Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly
225          230          235          240
Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr
          245          250          255
Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr

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260
Cys Tyr Val Asn Ser Gln Gln Pro Ser
275

265
Pro Ser
280

270

<210> 10
<211> 2725
<212> DNA
<213> Mus musculus

<400> 10
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tagagacagc aggaggctgg agatgaggct cggacagtga ggtgcatttt gtacaagcac 1560
gaggaatcta tatttgatcg tagacccac atgaaaaagc taggcctggt agagcatgct 1620
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<210> 11
<211> 281
<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> (1)...(281)

<223> TIM-3, C.D2 ES-HBA and DBA/2J allele

<400> 11

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 20           25           30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Ser Thr Pro Gly Ala Leu
 35           40           45
Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
 50           55           60
Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
 65           70           75           80
Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
 85           90           95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
 100          105          110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
 115          120          125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
 130          135          140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
 145          150          155          160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
 165          170          175
Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
 180          185          190
Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu
 195          200          205
Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys Lys
 210          215          220
Leu Ser Ser Leu Ser Leu Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly
 225          230          235          240
Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr
 245          250          255
Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr
 260          265          270
Cys Tyr Val Asn Ser Gln Gln Pro Ser
 275          280
```

<210> 12

<211> 862

<212> DNA

<213> Mus musculus

<400> 12

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cccccccaa gtactcatgt ttccaggtct taccctcaac tgtgtcctgc tgctgctgca 60
actactactt gcaaggtcat tggaaaatgc ttatgtgttt gaggttggtg agaatgccta 120
tctgccctgc agttacactc tatctacacc tggggcactt gtgcctatgt gctggggcaa 180
gggattctgt ccttggtcac agtgtaccaa cgagttgctc agaactgatg aaagaaatgt 240
gacatatcag aaatccagca gataccagct aaagggcgat ctcaacaaag gagacgtgtc 300
tctgatcata aagaatgtga ctctggatga ccatgggacc tactgctgca ggatacagtt 360
ccctggtctt atgaatgata aaaaattaga actgaaatta gacatcaaag cagccaaggt 420
cactccagct cagactgcc atggggactc tactacagct tctccaagaa ccctaaccac 480
ggagagaaat gggttcagaga cacagacact ggtgaccctc cataataaca atggaacaaa 540
```



```

aatttcacaca tgggctgatg aaattaagga ctctggagaa acgatcagaa ctgctatcca 600
cattggagtg ggagtcctctg ctgggttgac cctggcactt atcattggtg tcttaatcct 660
taaattggtat tctgtgaaga aaaagaagtt atcgagtttg agccttatta cactggccaa 720
cttgccctcca ggagggttg gaaatgcagg agcagtcagg attcgctctg aggaaaatat 780
ctacaccatc gaggagaacg tatatgaagt ggagaattca aatgagtact actgctacgt 840
caacagccag cagccatcct ga 862

```

```

<210> 13
<211> 345
<212> PRT
<213> Mus musculus

```

```

<220>
<221> VARIANT
<222> (1)...(345)
<223> TIM-4, BALB/c allele

```

```

<400> 13
Met Ser Lys Gly Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
1          5          10          15
Leu Tyr Leu Ser Lys Ser Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly
20          25          30
Phe Leu Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser
35          40          45
Gln Ser Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser
50          55          60
Lys Cys Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser
65          70          75          80
Arg Lys Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu
85          90          95
Val Ser Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr
100         105         110
Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn
115         120         125
Val Arg Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr
130         135         140
Thr Thr Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu
145         150         155         160
Leu Leu Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr
165         170         175
Pro Pro Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr
180         185         190
Cys Pro Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly
195         200         205
Ser Ala Ile Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser
210         215         220
Gln Arg Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro
225         230         235         240
Thr Gly Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr
245         250         255
Gln Lys Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys
260         265         270
Ser His Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys
275         280         285
Val Gly Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Leu Arg
290         295         300
Gly Lys Val Thr Gly Ala Asn Cys Leu Gln Arg His Lys Arg Pro Asp
305         310         315         320
Asn Thr Glu Val Ser Asp Ser Phe Leu Asn Asp Ile Ser His Gly Arg
325         330         335
Asp Asp Glu Asp Gly Ile Phe Thr Leu

```

<210> 14
 <211> 1032
 <212> DNA
 <213> Mus musculus

<400> 14
 atgtccaagg ggcttctcct cctctggctg gtgacggagc tctgggtggct ttatctgaca 60
 ccagctgcct cagaggatac aataataggg tttttggggc agccgggtgac tttgccttgt 120
 cattacctct cgtgggtcca gagccgcaac agtatgtgct ggggcaaagg ttcatgtccc 180
 aattccaagt gcaatgcaga gcttctccgt acagatggaa caagaatcat ctccaggaag 240
 tcaacaaaat atacactttt ggggaagggtc cagtttggtg aagtgtcctt gaccatctca 300
 aacaccaatc gaggtgacag tgggggtgtac tgctgccgta tagagggtgcc tggctgggttc 360
 aatgatgtca agaagaatgt gcgcttgagg ctgaggagag ccacaacaac caaaaaacca 420
 acaacaacca cccggccaac caccacccct tatgtaacca ccaccacccc agagctgctt 480
 ccaacaacag tcatgaccac atctgttctt ccaaccacca caccacccca gacactagcc 540
 accactgcct tcagtacagc agtgaccacg tgcccctcaa caacacctgg ctcttcttca 600
 caagaaacca caaaagggtc cgccatcact acagaatcag aaactctgcc tgcattccat 660
 cactctcaaa gaagcatgat gaccatatct acagacatag ccgtactcag gcccacaggc 720
 tctaaccctg ggattctccc atccacttca cagctgacga cacagaaaac aacattaaca 780
 acaagtgagt ctttgacaga gacaactaaa tcacatcaga tcaacagcag acagaccatc 840
 ttgatcattg cctgctgtgt gggatttgtg ctaatgggtg tattgtttct ggcgtttctc 900
 cttcgaggga aagtcacagg agccaactgt ttgcagagac acaagaggcc agacaacact 960
 gaagatagt acagcgtcct caatgacatg tcacacggga gggatgatga agacgggatc 1020
 ttcactctct ga 1032

<210> 15
 <211> 345
 <212> PRT
 <213> Mus musculus

<220>
 <221> VARIANT
 <222> (1)...(345)
 <223> C.D2 ES-HBA and DBA/2J allele

<400> 15
 Met Ser Lys Gly Leu Leu Leu Trp Leu Val Met Glu Leu Trp Trp
 1 5 10 15
 Leu Tyr Leu Ser Lys Ser Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly
 20 25 30
 Phe Leu Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser
 35 40 45
 Gln Ser Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser
 50 55 60
 Lys Cys Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser
 65 70 75 80
 Arg Lys Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu
 85 90 95
 Val Ser Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr
 100 105 110
 Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn
 115 120 125
 Val Arg Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr
 130 135 140
 Thr Thr Arg Pro Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu
 145 150 155 160
 Leu Leu Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr
 165 170 175

Pro	Pro	Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr			
			180					185					190					
Cys	Pro	Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly			
		195					200					205						
Ser	Ala	Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser			
		210				215					220							
Gln	Arg	Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro			
225					230				235						240			
Thr	Gly	Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr			
			245					250						255				
Gln	Lys	Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys			
			260					265					270					
Ser	His	Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys			
		275					280					285						
Val	Gly	Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Leu	Arg			
		290				295					300							
Gly	Lys	Val	Thr	Gly	Ala	Asn	Cys	Leu	Gln	Arg	His	Lys	Arg	Pro	Asp			
305					310					315					320			
Asn	Thr	Glu	Val	Ser	Asp	Ser	Phe	Leu	Asn	Asp	Ile	Ser	His	Gly	Arg			
			325					330						335				
Asp	Asp	Glu	Asp	Gly	Ile	Phe	Thr	Leu										
			340					345										

<210> 16
 <211> 1032
 <212> DNA
 <213> Mus musculus

<400> 16
 atgtccaagg ggcttctcct cctctggctg gtgatggagc tctgggtggct ttatctgaca 60
 ccagctgcct cagaggatac aataataggg tttttggggc agccggtgac tttgccttgt 120
 cattacctct cgtgggtccca gagccgcaac agtatgtgct ggggcaaagg ttcatgtccc 180
 aattccaagt gcaatgcaga gcttctccgt acagatggaa caagaatcat ctccaggaag 240
 tcaacaaaat atacactttt ggggaaggtc cagtttggtg aagtgtcctt gaccatctca 300
 aacaccaatc gaggtgacag tggggtgtac tgctgccgta tagagggtgc tggctgggtc 360
 aatgatgtca agaagaatgt gcgcttggag ctgaggagag ccacaacaac caaaaaacca 420
 acaacaacca cccggccaac caccaccct tatgtaacca ccaccacccc agagctgctt 480
 ccaacaacag tcatgaccac atctgttctt ccaaccacca caccaccca gacactagcc 540
 accactgcct tcagtacagc agtgaccacg tgcccctcaa caacacctgg ctcttctca 600
 caagaaacca caaaagggtc cgccttctact acagaatcag aaactctgcc tgcattcaat 660
 cactctcaaa gaagcatgat gaccatatct acagacatag ccgtactcag gccacaggc 720
 tctaaccctg ggattctccc atccacttca cagctgacga cacagaaaac aacattaaca 780
 acaagtgagt ctttgcagaa gacaactaaa tcacatcaga tcaacagcag acagaccatc 840
 ttgatcattg cctgctgtgt gggatttgtg ctaatggtgt tattgtttct ggcgtttctc 900
 cttcgaggga aagtcacagg agccaactgt ttgcagagac acaagaggcc agacaacact 960
 gaagatagt acagcgtcct caatgacatg tcacacggga gggatgatga agacgggatc 1020
 ttcactctct ga 1032

<210> 17
 <211> 359
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(360)
 <223> TIM-1 allele 1

<400> 17
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp

1	5	10	15
Ser Val Ala Gly	Ser Val Lys Val	Gly Glu Ala Gly	Pro Ser Val
20		25	30
Thr Leu Pro Cys	His Tyr Ser Gly	Ala Val Thr Ser	Met Cys Trp Asn
35	40	45	
Arg Gly Ser Cys	Ser Leu Phe Thr	Cys Gln Asn Gly	Ile Val Trp Thr
50	55	60	
Asn Gly Thr His	Val Thr Tyr Arg	Lys Asp Thr Arg	Tyr Lys Leu Leu
65	70	75	80
Gly Asp Leu Ser	Arg Arg Asp Val	Ser Leu Thr Ile	Glu Asn Thr Ala
	85	90	95
Val Ser Asp Ser	Gly Val Tyr Cys	Cys Arg Val Glu	His Arg Gly Trp
	100	105	110
Phe Asn Asp Met	Lys Ile Thr Val	Ser Leu Glu Ile	Val Pro Pro Lys
	115	120	125
Val Thr Thr Thr	Pro Ile Val Thr	Thr Val Pro Thr	Val Thr Thr Val
	130	135	140
Arg Thr Ser Thr	Thr Val Pro Thr	Thr Thr Thr Val	Pro Thr Thr Thr
	145	150	155
Val Pro Thr Thr	Met Ser Ile Pro	Thr Thr Thr Val	Pro Thr Thr Thr
	165	170	175
Met Thr Val Ser	Thr Thr Thr Ser	Val Pro Thr Thr	Thr Thr Ser Ile
	180	185	190
Thr Thr Thr Ser	Val Pro Val Thr	Thr Thr Thr Val	Ser Thr Phe Val
	195	200	205
Pro Met Pro Leu	Pro Arg Gln Asn	His Glu Pro Val	Ala Thr Ser Pro
	210	215	220
Ser Ser Pro Gln	Pro Ala Glu Thr	His Pro Thr Thr	Leu Gln Gly Ala
	225	230	235
Ile Arg Arg Glu	Pro Thr Ser Ser	Pro Leu Tyr Ser	Tyr Thr Thr Asp
	245	250	255
Gly Asn Asp Thr	Val Thr Glu Ser	Ser Asp Gly Leu	Trp Asn Asn Asn
	260	265	270
Gln Thr Gln Leu	Phe Leu Glu His	Ser Leu Leu Thr	Ala Asn Thr Thr
	275	280	285
Lys Gly Ile Tyr	Ala Gly Val Cys	Ile Ser Val Leu	Val Leu Leu Ala
	290	295	300
Leu Leu Gly Val	Ile Ile Ala Lys	Lys Tyr Phe Phe	Lys Lys Glu Val
	305	310	315
Gln Gln Leu Ser	Val Ser Phe Ser	Ser Leu Gln Ile	Lys Ala Leu Gln
	325	330	335
Asn Ala Val Glu	Lys Glu Val Gln	Ala Glu Asp Asn	Ile Tyr Ile Glu
	340	345	350
Asn Ser Leu Tyr	Ala Thr Asp		
	355		

<210> 18
 <211> 1080
 <212> DNA
 <213> H. sapiens

<400> 18
 atgcacccctc aagtgggtcat cttaagcctc atcctacatc tggcagattc tgtagctggt 60
 tctgtaaaagg ttggtggaga ggcaggtcca tctgtcacac taccctgcc ctacagtga 120
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtcgtacagt 300
 ggcgatatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420
 gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aacgacaact 480

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gttccaacaa caatgagcat tccaacgaca acgactgttc cgacgacaat gactgtttca 540
acgacaacga gcgttccaac gacaacgagc attccaacaa caacaagtgt tccagtgaac 600
acaacggtct ctacctttgt tcttccaatg cctttgccca ggcagaacca tgaaccagta 660
gccacttcac catcttcacc tcagccagca gaaacccacc ctacgacact gcagggagca 720
ataaggagag aaccaccagag ctaccatttg tactcttaca caacagatgg gaatgacacc 780
gtgacagagt cttcagatgg cctttggaat aacaatcaaa ctcaactgtt cctagaacat 840
agtctactga cggccaatac cactaaagga atctatgctg gagtctgtat ttctgtcttg 900
gtgtctcttg ctcttttggg tgtcatcatt gccaaaaagt atttcttcaa aaaggaggtt 960
caacaactaa gtgtttcatt tagcagcctt caaattaaag ctttgcaaaa tgcagttgaa 1020
aaggaagtcc aagcagaaga caatatctac attgagaata gtctttatgc cacggactaa 1080

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<210> 19
<211> 359
<212> PRT
<213> H. sapiens

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<220>
<221> VARIANT
<222> (1)...(359)
<223> TIM-1, allele 2

```

```

<400> 19
Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1          5          10          15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
          20          25          30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
          35          40          45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
          50          55          60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
          65          70          75          80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
          85          90          95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
          100          105          110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
          115          120          125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
          130          135          140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Thr Thr Thr
          145          150          155          160
Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Thr Val Pro Thr Thr
          165          170          175
Met Thr Val Ser Thr Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro
          180          185          190
Thr Thr Thr Ser Val Pro Val Thr Thr Ala Val Ser Thr Phe Val Pro
          195          200          205
Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro
          210          215          220
Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Ala
          225          230          235          240
Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp
          245          250          255
Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Asn Asn Asn
          260          265          270
Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr
          275          280          285
Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala
          290          295          300

```

Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val
 305 310 315 320
 Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln
 325 330 335
 Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu
 340 345 350
 Asn Ser Leu Tyr Ala Thr Asp
 355

<210> 20
 <211> 1080
 <212> DNA
 <213> H. sapiens

<400> 20
 atgcacccctc aagtgggtcat cttaagccctc atccctacatc tggcagattc tgtagctggt 60
 tctgttaaagg ttggtggaga ggcagggtcca tctgtcacac taccctgccac ctacagtggg 120
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300
 ggcgtatatt gttgccgtgt tgagcacctg ggggtggttca atgacatgaa aatcacgta 360
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaaac tgttccaacc 420
 gtcacgactg ttcgaacgag caccactggt ccaacgacaa cgactgttcc aacgacaact 480
 gttccaacaa caatgagcat tccaacgaca acgactgttc cgacgacaat gactgtttca 540
 acgacaacga gcgttccaac gacaacgagc attccaacaa caacaagtgt tccagtgaac 600
 acagcgggtc ctacctttgt tctccaatg cctttgcccc ggcagaacca tgaaccagta 660
 gccacttcac catcttcacc tcagccagca gaaacccacc ctacgacact gcagggagca 720
 ataaggagag aaccaccag ctcaccattg tactcttaca caacagatgg gaatgacacc 780
 gtgacagagt cttcagatgg cctttggaat aacaatcaaa ctcaactgtt cctagaacat 840
 agtctactga cggccaatac cactaaagga atctatgctg gagtctgtat ttctgtcttg 900
 gtgcttcttg ctcttttggg tgtcatcatt gccaaaaagt atttcttcaa aaaggagggt 960
 caacaactaa gtgtttcatt tagcagcctt caaattaaag ctttgcaaaa tgcagttgaa 1020
 aaggaagtcc aagcagaaga caatatctac attgagaata gtctttatgc cacggactaa 1080

<210> 21
 <211> 365
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(365)
 <223> TIM-1, allele 3

<400> 21
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1 5 10 15
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20 25 30
 Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
 35 40 45
 Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
 50 55 60
 Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
 65 70 75 80
 Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
 85 90 95
 Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
 100 105 110

Phe	Asn	Asp	Met	Lys	Ile	Thr	Val	Ser	Leu	Glu	Ile	Val	Pro	Pro	Lys
	115						120					125			
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val
	130					135						140			
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Thr	Val	Pro	Met	Thr	Thr
	145				150					155					160
Thr	Val	Pro	Thr	Thr	Thr	Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr
			165						170					175	
Thr	Thr	Val	Pro	Thr	Thr	Met	Thr	Val	Ser	Thr	Thr	Thr	Ser	Val	Pro
			180					185					190		
Thr	Thr	Thr	Ser	Ile	Pro	Thr	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Ala
			195				200					205			
Val	Ser	Thr	Phe	Val	Pro	Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu
	210					215					220				
Pro	Val	Ala	Thr	Ser	Pro	Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro
	225				230					235					240
Thr	Thr	Leu	Gln	Gly	Ala	Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu
				245					250					255	
Tyr	Ser	Tyr	Thr	Thr	Asp	Gly	Asn	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp
		260					265						270		
Gly	Leu	Trp	Asn	Asn	Asn	Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu
	275					280						285			
Leu	Thr	Ala	Asn	Thr	Thr	Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser
	290					295					300				
Val	Leu	Val	Leu	Leu	Ala	Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr
	305				310					315					320
Phe	Phe	Lys	Lys	Glu	Val	Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu
				325				330						335	
Gln	Ile	Lys	Ala	Leu	Gln	Asn	Ala	Val	Glu	Lys	Glu	Val	Gln	Ala	Glu
			340					345					350		
Asp	Asn	Ile	Tyr	Ile	Glu	Asn	Ser	Leu	Tyr	Ala	Thr	Asp			
	355						360					365			

<210> 22
 <211> 1098
 <212> DNA
 <213> H. sapiens

<400> 22
 atgcatcctc aagtgggtcat cttaagcctc atcctacatc tggcagattc tgtagctggt 60
 tctgtaaagg ttggtggaga ggcaggtcca tctgtcacac taccctgccca ctacagtggga 120
 gctgtcacat caatgtgctg gaatagaggc tcatgtttctc tattcacatg ccaaaatggc 180
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300
 ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420
 gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aatgacaacg 480
 actgttccaa cgacaactgt tccaacaaca atgagcattc caacgacaac gactgttccg 540
 acgacaatga ctgtttcaac gacaacgagc gttccaacga caacgagcat tccaacaaca 600
 acaagtgttc cagtgcacaac arcggtctct acctttgttc ctccaatgcc tttgcccagg 660
 cagaacctatg aaccagtagc cacttcacca tcttcacctc agccagcaga aaccaccct 720
 acgacactgc agggagcaat aaggagagaa cccaccagct caccattgta ctcttacaca 780
 acagatggga atgacaccgt gacagagtct tcagatggcc tttggaataa caatcaaact 840
 caactgttcc tagaacatag tctactgacg gccaatacca cttaaaggaa ctatgctgga 900
 gtctgtatct ctgtcttggt gcttcttgct cttttgggtg tcatcattgc caaaaagtat 960
 ttcttcaaaa aggaggttca acaactaagt gtttcattta gcagccttca aattaaagct 1020
 ttgcaaaatg cagttgaaaa ggaagtccaa gcagaagaca atatctacat tgagaatagt 1080
 ctttatgccca cggactaa 1098

<210> 23

<211> 359
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(359)
 <223> TIM-1, allele 4

<400> 23

Met	His	Pro	Gln	Val	Val	Ile	Leu	Ser	Leu	Ile	Leu	His	Leu	Ala	Asp
1				5					10					15	
Ser	Val	Ala	Gly	Ser	Val	Lys	Val	Gly	Gly	Glu	Ala	Gly	Pro	Ser	Val
		20						25					30		
Thr	Leu	Pro	Cys	His	Tyr	Ser	Gly	Ala	Val	Thr	Ser	Met	Cys	Trp	Asn
		35					40					45			
Arg	Gly	Ser	Cys	Ser	Leu	Phe	Thr	Cys	Gln	Asn	Gly	Ile	Val	Trp	Thr
	50					55					60				
Asn	Gly	Thr	His	Val	Thr	Tyr	Arg	Lys	Asp	Thr	Arg	Tyr	Lys	Leu	Leu
65					70					75				80	
Gly	Asp	Leu	Ser	Arg	Arg	Asp	Val	Ser	Leu	Thr	Ile	Glu	Asn	Thr	Ala
				85					90					95	
Val	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys	Arg	Val	Glu	His	Arg	Gly	Trp
			100					105					110		
Phe	Asn	Asp	Met	Lys	Ile	Thr	Val	Ser	Leu	Glu	Ile	Val	Pro	Pro	Lys
	115						120					125			
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val
	130					135					140				
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Thr	Val	Pro	Thr	Thr	Thr
145					150					155				160	
Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr	Thr	Thr	Val	Pro	Thr	Thr
				165					170					175	
Met	Thr	Val	Ser	Thr	Thr	Thr	Ser	Val	Pro	Thr	Thr	Thr	Ser	Ile	Pro
			180					185					190		
Thr	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Ser	Val	Ser	Thr	Phe	Val	Pro
	195						200					205			
Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu	Pro	Val	Ala	Thr	Ser	Pro
	210					215					220				
Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro	Thr	Thr	Leu	Gln	Gly	Thr
225					230					235				240	
Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu	Tyr	Ser	Tyr	Thr	Thr	Asp
				245					250					255	
Gly	Asn	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp	Gly	Leu	Trp	Ser	Asn	Asn
	260						265					270			
Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu	Leu	Thr	Ala	Asn	Thr	Thr
	275					280						285			
Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser	Val	Leu	Val	Leu	Leu	Ala
	290				295						300				
Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr	Phe	Phe	Lys	Lys	Glu	Val
305					310					315				320	
Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu	Gln	Ile	Lys	Ala	Leu	Gln
				325					330					335	
Asn	Ala	Val	Glu	Lys	Glu	Val	Gln	Ala	Glu	Asp	Asn	Ile	Tyr	Ile	Glu
			340					345					350		
Asn	Ser	Leu	Tyr	Ala	Thr	Asp									
		355													

<210> 24
 <211> 1079
 <212> DNA

<213> H. sapiens

<400> 24

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atgcatcctc aagtgggtcat ctttaagcctc atcctacatc tggcagattc tgtagctggt 60
tctgtaaagg ttggtggaga ggcaggtcca tctgtcacac taccctgcc a ctacagtgga 120
gctgtcacat caatgtgctg gaatagaggc tcatgtttctc tattcacatg ccaaaatggc 180
attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300
ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360
tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420
gtcacgactg ttcgaacgag caccactggt ccaacgacaa cgactgttcc aacgacaact 480
gttccaacaa caatgagcat tccaacgaca acggactggt ccgacgacaa tgactgtttc 540
aacgacaacg agcgtttccaa cgacaacgag cattccaaca acaacaagtg ttccagtga 600
aacatgtctc tacctttgtt cctccaatgc ctttgcccag gcagaacat gaaccagtag 660
ccacttcacc atcttcacct cagccagcag aaacccaccc tacgacactg caggagacaa 720
taaggagaga acccaccagc tcaccattgt actcttacac aacagatggg aatgacaccg 780
tgacagagtc ttcagatggc ctttgarta acaatcaaac tcaactgttc ctagaacata 840
gtctactgac ggccaatacc actaaaggaa tctatgctgg agtctgtatt tctgtcttgg 900
tgcttcttgc tcttttgggt gtcattcattg ccaaaaagta tttcttcaaa aaggaggttc 960
aacaactaag tgtttcattt agcagccttc aaattaaagc tttgcaaaat gcagttgaaa 1020
aggaagtcca agcagaagac aatatctaca ttgagaatag tctttatgcc acggactaa 1079
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<210> 25

<211> 364

<212> PRT

<213> H. sapiens

<220>

<221> VARIANT

<222> (1)...(364)

<223> TIM-1 allele 5

<400> 25

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Met His Pro Gln Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1          5          10          15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20          25          30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
 35          40          45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
 50          55          60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
 65          70          75          80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
 85          90          95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100          105          110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
115          120          125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130          135          140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Met Thr Thr
145          150          155          160
Thr Val Pro Thr Thr Val Pro Thr Thr Met Ser Ile Pro Thr Thr
165          170          175
Thr Thr Val Pro Thr Thr Met Thr Val Ser Thr Thr Thr Ser Val Pro
180          185          190
Thr Thr Thr Ser Ile Pro Thr Thr Ser Val Pro Val Thr Thr Thr Val
195          200          205
Ser Thr Phe Val Pro Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro
210          215          220
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Val	Ala	Thr	Ser	Pro	Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro	Thr
225					230					235					240
Thr	Leu	Gln	Gly	Ala	Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu	Tyr
				245						250					255
Ser	Tyr	Thr	Thr	Asp	Gly	Asn	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp	Gly
				260						265					270
Leu	Trp	Asn	Asn	Asn	Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu	Leu
				275						280					285
Thr	Ala	Asn	Thr	Thr	Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser	Val
				290						295					300
Leu	Val	Leu	Leu	Ala	Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr	Phe
305															320
Phe	Lys	Lys	Glu	Val	Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu	Gln
				325						330					335
Ile	Lys	Ala	Leu	Gln	Asn	Ala	Val	Glu	Lys	Glu	Val	Gln	Ala	Glu	Asp
				340						345					350
Asn	Ile	Tyr	Ile	Glu	Asn	Ser	Leu	Tyr	Ala	Thr	Asp				
				355						360					

<210> 26
 <211> 1095
 <212> DNA
 <213> H. sapiens

<400> 26
 atgcatacctc aagtgggtcat cttaagcctc atcctacatc tggcagattc tgtagctggt 60
 tctgtaaagg ttggtggaga ggcaggtcca tctgtcacac taccctgccca ctacagtggga 120
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300
 ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420
 gtcacgactg ttcgaacgag caccactggt ccaacgacaa cgactgttcc aatgacaacg 480
 actgttccaa cgacaactgt tccaacaaca atgagcattc caacgacaac gactgttccg 540
 acgacaatga ctgtttcaac gacaacgagc gttccaacga caacgagcat tccaacaaca 600
 agtgttccag tgacaacaac ggtctctacc tttgttctc caatgccttt gccaggcag 660
 aaccatgaac cagtagccac ttcaccatct tcacctcagc cagcagaaac ccaccctacg 720
 acactgcagg gagcaataag gagagaaccc accagctcac cattgtactc ttacacaaca 780
 gatgggaatg acaccgtgac agagtcttca gatggccttt ggaataacaa tcaaaactcaa 840
 ctgttcttag aacatagtct actgacggcc aataccacta aaggaatcta tgctggagtc 900
 tgtatttctg tcttgggtgct tcttgtctct ttgggtgtca tcattgccaa aaagtatttc 960
 ttcaaaaagg aggttcaaca actaagtgtt tcatttagca gccttcaaat taaagctttg 1020
 caaaatgcag ttgaaaagga agtccaagca gaagacaata tctacattga gaatagtctt 1080
 tatgccacgg actaa 1095

<210> 27
 <211> 364
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(364)
 <223> TIM-1, allele 6

<400> 27
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1 5 10 15
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20 25 30

Thr	Leu	Pro	Cys	His	Tyr	Ser	Gly	Ala	Val	Thr	Ser	Met	Cys	Trp	Asn	
		35					40					45				
Arg	Gly	Ser	Cys	Ser	Leu	Phe	Thr	Cys	Gln	Asn	Gly	Ile	Val	Trp	Thr	
	50					55					60					
Asn	Gly	Thr	His	Val	Thr	Tyr	Arg	Lys	Asp	Thr	Arg	Tyr	Lys	Leu	Leu	
	65				70					75					80	
Gly	Asp	Leu	Ser	Arg	Arg	Asp	Val	Ser	Leu	Thr	Ile	Glu	Asn	Thr	Ala	
				85					90					95		
Val	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys	Arg	Val	Glu	His	Arg	Gly	Trp	
		100					105						110			
Phe	Asn	Asp	Met	Lys	Ile	Thr	Val	Ser	Leu	Gly	Ile	Val	Pro	Pro	Lys	
	115					120						125				
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val	
	130					135					140					
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Thr	Val	Pro	Met	Thr	Thr	
	145				150					155					160	
Thr	Val	Pro	Thr	Thr	Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr		
			165					170						175		
Thr	Thr	Val	Pro	Thr	Thr	Met	Thr	Val	Ser	Thr	Thr	Thr	Ser	Val	Pro	
		180					185						190			
Thr	Thr	Thr	Ser	Ile	Pro	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Thr	Val	
	195					200					205					
Ser	Thr	Phe	Val	Pro	Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu	Pro	
	210					215					220					
Val	Ala	Thr	Ser	Pro	Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro	Thr	
	225				230					235					240	
Thr	Leu	Gln	Gly	Ala	Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu	Tyr	
			245					250						255		
Ser	Tyr	Thr	Thr	Asp	Gly	Asp	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp	Gly	
		260				265							270			
Leu	Trp	Asn	Asn	Asn	Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu	Leu	
	275					280						285				
Thr	Ala	Asn	Thr	Thr	Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser	Val	
	290				295						300					
Leu	Val	Leu	Leu	Ala	Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr	Phe	
	305				310					315					320	
Phe	Lys	Lys	Glu	Val	Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu	Gln	
			325						330					335		
Ile	Lys	Ala	Leu	Gln	Asn	Ala	Val	Glu	Lys	Glu	Val	Gln	Ala	Glu	Asp	
		340						345					350			
Asn	Ile	Tyr	Ile	Glu	Asn	Ser	Leu	Tyr	Ala	Thr	Asp					
	355						360									

<210> 28
 <211> 1099
 <212> DNA
 <213> H. sapiens

<400> 28
 atgcacccctc aagtgggtcat cttaagcctc atcctacatc tggcagattc tgtagctggt 60
 tctgtaaagg ttggtggaga ggcaggtcca tctgtcacac taccctgccca ctacagtggg 120
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300
 ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420
 gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aatgacaacc 480
 gactgttcca acgacaactg ttccaacaac aatgagcatt ccaacgacaa cgactgttcc 540
 gacgacaatg actgtttcaa cgacaacgag cgttccaacg acaacgagca ttccaacaac 600
 aacaagtgtt ccagtgcaca caacggtctc tacctttgtt cctccaatgc ctttgcccag 660

gcagaacccat gaaccagtag ccacttcacc atcttcacct cagccagcag aaacccaccc 720
 tacgacactg cagggagcaa taaggagaga acccaccagc tcaccattgt actcttacac 780
 aacagatggg gatgacaccg tgacagagtc ttcagatggc ctttggaata acaatcaaac 840
 tcaactgttc ctagaacata gtctactgac ggccaatacc actaaaggaa tctatgctgg 900
 agtctgtatt tctgtcttgg tgcttcttgc tcttttgggt gtcattcattg ccaaaaagta 960
 tttcttcaaaa aaggagggttc aacaactaag tgtttcattt agcagccttc aaattaaagc 1020
 tttgcaaaat gcagttgaaa aggaagtcca agcagaagac aatatctaca ttgagaatag 1080
 tctttatgcc acggactaa 1099

<210> 29
 <211> 301
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(301)
 <223> TIM-3, allele 1

<400> 29
 Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
 20 25 30
 Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
 35 40 45
 Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
 50 55 60
 Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
 65 70 75 80
 Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
 85 90 95
 Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
 100 105 110
 Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
 115 120 125
 Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
 130 135 140
 Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
 145 150 155 160
 Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
 165 170 175
 Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
 180 185 190
 Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
 195 200 205
 Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe
 210 215 220
 Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile
 225 230 235 240
 Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu
 245 250 255
 Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr
 260 265 270
 Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln
 275 280 285
 Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
 290 295 300

<210> 30

<211> 1116
 <212> DNA
 <213> H. sapiens

<400> 30
 ggagaggttaa aactgtgcct aacagaggtg tcctctgact tttcttctgc aagctccatg 60
 ttttcacatc ttccctttga ctgtgtcctg ctgctgctgc tgctactact tacaagggtcc 120
 tcagaagtgg aatacagagc ggaggtcggt cagaatgcct atctgccctg cttctacacc 180
 ccagccgccc cagggaaacct cgtgcccgtc tgctggggca aaggagcctg tcctgtgttt 240
 gaatgtggca acgtggtgct caggactgat gaaagggatg tgaattattg gacatccaga 300
 tactggctaa atggggattt ccgcaaagga gatgtgtccc tgaccataga gaatgtgact 360
 ctagcagaca gtgggatcta ctgctgccgg atccaaatcc caggcataat gaatgatgaa 420
 aaattttaacc tgaagttggg catcaaacca gccaaaggtca cccctgcacc gactctgcag 480
 agagacttca ctgcagcctt tccaaggatg cttaccacca ggggacatgg cccagcagag 540
 acacagacac tggggagcct ccctgatata aatctaacac aaatatccac attggccaat 600
 gagttacggg actctagatt ggccaatgac ttacgggact ctggagcaac catcagaata 660
 ggcattctaca tcggagcagg gatctgtgct gggctggctc tggctcttat cttcggcgct 720
 ttaattttca aatggtattc tcatagcaaa gagaagatac agaatttaag cctcatctct 780
 ttggccaacc tccctccctc aggattggca aatgcagtag cagagggaat tcgctcagaa 840
 gaaaacatct ataccattga agagaacgta tatgaagtgg aggagcccaa tgagtattat 900
 tgctatgtca gcagcaggca gcaaccctca caacctttgg gttgtcgctt tgcaatgcca 960
 tagatccaac caccttattt ttgagcttgg tgttttgcct ttttcagaaa ctatgagctg 1020
 tgtcacctga ctggttttgg aggttctgtc cactgctatg gagcagagtt ttcccatttt 1080
 cagaagataa tgactcacat ggggaattgaa ctggga 1116

<210> 31
 <211> 301
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(301)
 <223> TIM-3, allele 2

<400> 31
 Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
 20 25 30
 Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
 35 40 45
 Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
 50 55 60
 Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
 65 70 75 80
 Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
 85 90 95
 Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
 100 105 110
 Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
 115 120 125
 Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Leu Gln Arg Asp Phe
 130 135 140
 Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
 145 150 155 160
 Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
 165 170 175
 Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
 180 185 190
 Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly

65					70					75				80	
Ser	Ala	Lys	Tyr	Arg	Leu	Gln	Gly	Thr	Ile	Pro	Arg	Gly	Asp	Val	Ser
				85					90					95	
Leu	Thr	Ile	Leu	Asn	Pro	Ser	Glu	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys
			100					105					110		
Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe	Asn	Asp	Val	Lys	Ile	Asn	Val	Arg
		115					120					125			
Leu	Asn	Leu	Gln	Arg	Ala	Ser	Thr	Thr	Thr	His	Arg	Thr	Ala	Thr	Thr
	130					135					140				
Thr	Thr	Arg	Arg	Thr	Thr	Thr	Thr	Ser	Pro	Thr	Thr	Thr	Arg	Gln	Met
145						150				155					160
Thr	Thr	Thr	Pro	Ala	Ala	Leu	Pro	Thr	Thr	Val	Val	Thr	Thr	Pro	Asp
			165					170						175	
Leu	Thr	Thr	Gly	Thr	Pro	Leu	Gln	Met	Thr	Thr	Ile	Ala	Val	Phe	Thr
			180					185					190		
Thr	Ala	Asn	Thr	Cys	Leu	Ser	Leu	Thr	Pro	Ser	Thr	Leu	Pro	Glu	Glu
	195						200					205			
Ala	Thr	Gly	Leu	Leu	Thr	Pro	Glu	Pro	Ser	Lys	Glu	Gly	Pro	Ile	Leu
	210					215					220				
Thr	Ala	Glu	Ser	Glu	Thr	Val	Leu	Pro	Ser	Asp	Ser	Trp	Ser	Ser	Ala
225						230				235					240
Glu	Ser	Thr	Ser	Ala	Asp	Thr	Val	Leu	Leu	Thr	Ser	Lys	Glu	Ser	Lys
			245					250					255		
Val	Trp	Asp	Leu	Pro	Ser	Thr	Ser	His	Val	Ser	Met	Trp	Lys	Thr	Ser
			260					265					270		
Asp	Ser	Val	Ser	Ser	Pro	Gln	Pro	Gly	Ala	Ser	Asp	Thr	Ala	Val	Pro
		275					280					285			
Glu	Gln	Asn	Lys	Thr	Thr	Lys	Thr	Gly	Gln	Met	Asp	Gly	Ile	Pro	Met
	290					295				300					
Ser	Met	Lys	Asn	Glu	Met	Pro	Ile	Ser	Gln	Leu	Leu	Met	Ile	Ile	Ala
305					310					315					320
Pro	Ser	Leu	Gly	Phe	Val	Leu	Phe	Ala	Leu	Phe	Val	Ala	Phe	Leu	Leu
			325					330					335		
Arg	Gly	Lys	Leu	Met	Glu	Thr	Tyr	Cys	Ser	Gln	Lys	His	Thr	Arg	Leu
			340					345					350		
Asp	Tyr	Ile	Gly	Asp	Ser	Lys	Asn	Val	Leu	Asn	Asp	Val	Gln	His	Gly
	355						360					365			
Arg	Glu	Asp	Glu	Asp	Gly	Leu	Phe	Thr	Leu						
	370					375									

<210> 34
 <211> 1156
 <212> DNA
 <213> H. sapiens

<400> 34
 atgtccaaag aacctctcat tctctggctg atgattgagt tttggtggct ttacctgaca 60
 ccagtcactt cagagactgt tgtgacggag gttttgggtc accgggtgac tttgccctgt 120
 ctgtactcat cctggtctca caacagcaac agcatgtgct gggggaaaga ccagtgcccc 180
 tactccggtt gcaaggaggc gtcacatccgc actgatggaa tgagggtgac ctcaagaaag 240
 tcagcaaaat atagacttca ggggactatc ccgagagggtg atgtctcctt gaccatctta 300
 aaccccagtg aaagtgacag cgggtgtgtac tgctgcccga tagaagtgcc tggtgtgttc 360
 aacgatgtaa agataaacgt gcgcctgaat ctacagagag cctcaacaac cagcacaga 420
 acagcaacca ccaccacacg cagaacaaca acaacaagcc ccaccaccac ccgacaaatg 480
 acaacaaccc cagctgcact tccaacaaca gtcgtgacca caccgatct cacaaccgga 540
 acaccactcc agatgacaac cattgccgtc ttcacaacag caaacacgtg ccttttacta 600
 accccaagca cccttcggga ggaagccaca ggtcttctga ctcccagacc ttctaaggaa 660
 gggcccatcc tcactgcaga atcagaaact gtcctcccca gtgattcctg gactagtgtc 720
 gagtctactt ctgctgacac tgtcctgctg acatccaaag agtccaaagt ttgggatctc 780
 ccatcaacat cccacgtgtc aatgtggaaa acgagtgtt ctgtgtcttc tcctcagcct 840

ggagcatctg atacagcagt tcctgagcag aacaaaacaa caaaaacagg acagatggat 900
 ggaataccca tgtcaatgaa gaatgaaatg cccatctccc aactactgat gatcatcgcc 960
 ccctccttgg gatttgtgct cticgcattg tttgtggcgt ttctcctgag agggaaactc 1020
 atggaaacct attgttcgca gaaacacaca aggctagact acattggaga tagtaaaaat 1080
 gtcctcaatg acgtgcagca tggaagggaa gacgaagacg gcctttttac cctctaacaa 1140
 cgcagtagca tgttag 1156

<210> 35
 <211> 378
 <212> PRT
 <213> H. sapiens

<220>
 <221> VARIANT
 <222> (1)...(378)
 <223> TIM-4, allele 2

<400> 35
 Met Ser Lys Glu Pro Leu Ile Leu Trp Leu Met Ile Glu Phe Trp Trp
 1 5 10 15
 Leu Tyr Leu Thr Pro Val Thr Ser Glu Thr Val Val Thr Glu Val Leu
 20 25 30
 Gly His Arg Val Thr Leu Pro Cys Leu Tyr Ser Ser Trp Ser His Asn
 35 40 45
 Ser Asn Ser Met Cys Trp Gly Lys Asp Gln Cys Pro Tyr Ser Gly Cys
 50 55 60
 Lys Glu Ala Leu Ile Arg Thr Asp Gly Met Arg Val Thr Ser Arg Lys
 65 70 75 80
 Ser Ala Lys Tyr Arg Leu Gln Gly Thr Ile Pro Arg Gly Asp Val Ser
 85 90 95
 Leu Thr Ile Leu Asn Pro Ser Glu Ser Asp Ser Gly Val Tyr Cys Cys
 100 105 110
 Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Ile Asn Val Arg
 115 120 125
 Leu Asn Leu Gln Arg Ala Ser Thr Thr Thr His Arg Thr Ala Thr Thr
 130 135 140
 Thr Thr Arg Arg Thr Thr Thr Ser Pro Thr Thr Thr Arg Gln Met
 145 150 155 160
 Thr Thr Thr Pro Ala Leu Pro Thr Thr Val Val Thr Thr Pro Asp
 165 170 175
 Leu Thr Thr Gly Thr Pro Leu Gln Met Thr Thr Ile Ala Val Phe Thr
 180 185 190
 Thr Ala Asn Thr Cys Leu Ser Leu Thr Pro Ser Thr Leu Pro Glu Glu
 195 200 205
 Ala Thr Gly Leu Leu Thr Pro Glu Pro Ser Lys Glu Gly Pro Ile Leu
 210 215 220
 Thr Ala Glu Ser Glu Thr Val Leu Pro Ser Asp Ser Trp Ser Ser Val
 225 230 235 240
 Glu Ser Thr Ser Ala Asp Thr Val Leu Leu Thr Ser Lys Glu Ser Lys
 245 250 255
 Val Trp Asp Leu Pro Ser Thr Ser His Val Ser Met Trp Lys Thr Ser
 260 265 270
 Asp Ser Val Ser Ser Pro Gln Pro Gly Ala Ser Asp Thr Ala Val Pro
 275 280 285
 Glu Gln Asn Lys Thr Thr Lys Thr Gly Gln Met Asp Gly Ile Pro Met
 290 295 300
 Ser Met Lys Asn Glu Met Pro Ile Ser Gln Leu Leu Met Ile Ile Ala
 305 310 315 320
 Pro Ser Leu Gly Phe Val Leu Phe Ala Leu Phe Val Ala Phe Leu Leu
 325 330 335
 Arg Gly Lys Leu Met Glu Thr Tyr Cys Ser Gln Lys His Thr Arg Leu

	340		345		350
Asp	Tyr Ile Gly Asp Ser Lys Asn Val Leu Asn Asp Val Gln His Gly				
	355		360		365
Arg Glu Asp Glu Asp Gly Leu Phe Thr Leu					
370		375			

<210> 36
 <211> 1156
 <212> DNA
 <213> H. sapiens

<400> 36

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ccagtcactt	cagagactgt	tgtgacggag	gtttttgggtc	accgggtgac	tttgcctgt	120
ctgtactcat	cctgggtctca	caacagcaac	agcatgtgct	gggggaaaga	ccagtgcctc	180
tactccggtt	gcaaggaggc	gtcatccgc	actgatggaa	tgagggtgac	ctcaagaaag	240
tcagcaaaat	atagacttca	ggggactatc	ccgagagggtg	atgtctcctt	gaccatctta	300
aaccccgagt	aaagtgacag	cggtgtgtac	tgctgcccga	tagaagtgcc	tggttggttc	360
aacgatgtaa	agataaacgt	gcgcctgaat	ctacagagag	cctcaacaac	cacgcacaga	420
acagcaacca	ccaccacacg	cagaacaaca	acaacaagcc	ccaccaccac	ccgacaaatg	480
acaacaaccc	cagctgcact	tccaacaaca	gtcgtgacca	caccgatct	cacaaccgga	540
acaccactcc	agatgacaac	cattggcgtc	ttcacaacag	caaacacgtg	ccttttacta	600
accccaagca	cccttccgga	ggaagccaca	ggtcttctga	ctcccagacc	ttctaaggaa	660
gggcccattc	tactgcaga	atcagaaact	gtcctcccca	gtgattcctg	gagtagtggt	720
gagtctactt	ctgctgacac	tgtcctgctg	acatccaaag	agtccaaagt	ttgggatctc	780
ccatcaacat	cccacgtgtc	aatgtggaaa	acgagtgatt	ctgtgtcttc	tcctcagcct	840
ggagcatctg	atacagcagt	tcctgagcag	aacaaaacaa	caaaaacagg	acagatggat	900
ggaataccca	tgtcaatgaa	gaatgaaatg	cccatctccc	aactactgat	gatcatcgcc	960
ccctccttgg	gatttgtgct	cttcgcattg	tttgtggcgt	ttctcctgag	agggaaactc	1020
atggaaacct	attgttcgca	gaaacacaca	aggctagact	acattggaga	tagtaaaaat	1080
gtcctcaatg	acgtgcagca	tggaagggaa	gacgaagacg	gcctttttac	cctctaacaa	1140
cgcagtagca	tgtag					1156

<210> 37
 <211> 481
 <212> DNA
 <213> H. sapiens

<220>
 <221> exon
 <222> (152)...(430)
 <223> Exon 3, reference sequence

<400> 37

ttctagctgg	gcaatgacca	agattgacag	ttcaggaagt	taactccacc	tagggacagt	60
ctgtcattgg	tgtgctaggg	tacagttcca	gcctgaggct	cttgtttctt	gtttgactta	120
tgctcactct	catgttgatt	tctgactcca	gccaagggtca	cgactactcc	aattgtcaca	180
actgttccaa	ccgtcacgac	tggtcgaacg	agcaccactg	ttccaacgac	aacgactgtt	240
ccaacgacaa	ctgttccaac	aacaatgagc	attccaacga	caacgactgt	tctgacgaca	300
atgactgttt	caacgacaac	gagcgttcca	acgacaacga	gcattccaac	aacaacaagt	360
gttccagtga	caacaactgt	ctctaccttt	gttcttccaa	tgcttttgcc	caggcagaac	420
catgaaccag	gtaaaacaga	tgtgttttga	agcccaaagg	ccttctaata	aggagctgcg	480
g						481

<210> 38
 <211> 499
 <212> DNA
 <213> H. sapiens

<220>

<221> exon
 <222> (152)...(448)
 <223> Exon 3, INS157 polymorphism

<400> 38
 ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
 ctgtcattgg tgtgctaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
 tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
 actgtttccaa ccgtcacgac tgttcgaacg agcaccactg ttccaacgac aacgactgtt 240
 ccaatgacaa cgactgttcc aacgacaact gttccaacaa caatgagcat tccaacgaca 300
 acgactgttc tgacgacaat gactgtttca acgacaacga gcgttccaac gacaacgagc 360
 attccaacaa caacaagtgt tccagtgaaca acaactgtct ctacctttgt tctccaatg 420
 cctttgcccc ggcagaacca tgaaccagggt aaaacagatg tgtttggaag cccaaaggcc 480
 ttctaatagg gagctgcgg 499

<210> 39
 <211> 496
 <212> DNA
 <213> H. sapiens

<220>
 <221> exon
 <222> (152)...(445)
 <223> Exon 3, 195delT polymorphism

<400> 39
 ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
 ctgtcattgg tgtgctaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
 tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
 actgtttccaa ccgtcacgac tgttcgaacg agcaccactg ttccaacgac aacgactgtt 240
 ccaatgacaa cgactgttcc aacgacaact gttccaacaa caatgagcat tccaacgaca 300
 acgactgttc tgacgacaat gactgtttca acgacaacga gcgttccaac gacaacgagc 360
 attccaacaa caagtgttcc agtgacaaca actgtctcta cctttgttcc tccaatgcct 420
 ttgcccaggc agaaccatga accaggtaaa acagatgtgt ttggaagccc aaaggccttc 480
 taatgaggag ctgcgg 496

<210> 40
 <211> 496
 <212> DNA
 <213> H. sapiens

<220>
 <221> exon
 <222> (152)...(445)
 <223> Exon 3, 157insMTTVP polymorphism

<400> 40
 ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
 ctgtcattgg tgtgctaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
 tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
 actgtttccaa ccgtcacgac tgttcgaacg agcaccactg ttccaacgac aacgactgtt 240
 ccaatgacga ctgtttccaac gacaactgtt ccaacaacaa tgagcattcc aacgacaacg 300
 actgtttctga cgacaatgac tgtttcaacg acaacgagcg ttccaacgac aacgagcatt 360
 ccaacaacaa caagtgttcc agtgacaaca actgtctcta cctttgttcc tccaatgcct 420
 ttgcccaggc agaaccatga accaggtaaa acagatgtgt ttggaagccc aaaggccttc 480
 taatgaggag ctgcgg 496

<210> 41
 <211> 18
 <212> DNA

<213> H. sapiens
 <400> 41
 gtgtctgaca gtggcgta 18
 <210> 42
 <211> 18
 <212> DNA
 <213> H. sapiens
 <400> 42
 ttgcccagg cagaacca 18
 <210> 43
 <211> 18
 <212> DNA
 <213> H. sapiens
 <400> 43
 ccaccaagg tcacgact 18
 <210> 44
 <211> 18
 <212> DNA
 <213> H. sapiens
 <400> 44
 atgccacgga ctaagacc 18
 <210> 45
 <211> 41
 <212> DNA
 <213> H. sapiens
 <400> 45
 ggaattcgtc gaccaccatg catcctcaag tggatcatctt a 41
 <210> 46
 <211> 42
 <212> DNA
 <213> H. sapiens
 <400> 46
 ggaattcgcg gccgctcatt agtcggtggc ataaacagta tt 42
 <210> 47
 <211> 20
 <212> DNA
 <213> H. sapiens
 <400> 47
 tcaagtggtc atcttaagcc 20
 <210> 48
 <211> 22
 <212> DNA
 <213> H. sapiens
 <400> 48
 taaactctca aagagcacca ct 22

<210> 49
 <211> 22
 <212> DNA
 <213> H. sapiens

 <400> 49
 acagactcca gcatagattc ct 22

 <210> 50
 <211> 22
 <212> DNA
 <213> H. sapiens

 <400> 50
 gcaccaagac agaaatacag ac 22

 <210> 51
 <211> 31
 <212> DNA
 <213> H. sapiens

 <400> 51
 agaagcaccc aagacagaaa tacagactcc a 31

 <210> 52
 <211> 19
 <212> DNA
 <213> H. sapiens

 <400> 52
 ttctagctgg gcaatgacc 19

 <210> 53
 <211> 20
 <212> DNA
 <213> H. sapiens

 <400> 53
 ccgcagctcc tcattagaag 20